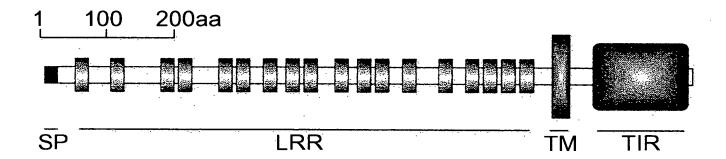
	-5	4	AG	CTG	CGG	ccc	GGT	CTG	CCA	.GCC	AGA	CCC	TTT	'GGA	GAA	GAC	:CCC	ACT	CCC	TGTC	
1	AT	GGG	∞	CCG	CIG	CAC	CCT	GCA	.CCC	CCI	TTC	TCT	CCI	GGI	GCA	.GGT	GAC	AGC	GCT	GGCT	60
	M	G	Р	R	С	T	L	Н	P	L	S	L	L	V	Q	V	T	A	L	A	
61	GC	GAC	ICT	GGO	CCA	.GGG	CAG	GCI	'GCC	TGC	CTT	CCT	GCC	CTG	TGA	GCI	CCA	.GCC	CCA	CGGC	120
	A	T	L	A	Q	G	R	L	P	A	F	L	P	C	E	L	Q	P	Н	G	
121	CT	GGT	GAA	CTG	CAA	CTG	GCT	CTT	CCT	GAA	GTC	CGT	GCC	CCA	CTI	CTC	GGC	GGC	AGC	CCC	180
	L	V	N	С	N	M	L	F	L	K	S	V	P	Н	F	S	A	A	A	P	
181	Œ	GGC(CAA	CGT	CAC	CAG	CCT	CTC	CTT	ACT	CTC	CAA	.CCG	CAT	CCA	CCA	CTI	GCA	CGA	CTCT	240
	R	A	N	A	T	S	L	S	L	L	S	N	R	Ι	Н	Н	L	Н	D	S	
241	GA(CTT(ŒT	CCA	CCT	GTC	CAG	CCT	'ACG	AAC	TCT	CAA	CCT	CAA	GTG	GAA	CTG		GCO	GGCT	300
	D	F	V	Н	L	S	S	L	R	T	L	N	L	K	M	N	С	P	P	A	
301	GG	CCT	CAG	CCO	CAT	GCA	CTT	CCC	CTG	CCA	CAT	GAC	CAT	CGA	.GCC	CAA	CAC	CTT	CCT	GGCC	360
	G	L	S	P	M	Н	F	P	С	Н	M	T	Ι	E	P	N	T	F	L	A	
361	GT	GCC	CAC	CCT	GGA	GGA	GCT	GAA	CCT	GAG	CTA	CAA	CAG	CAT	CAC	GAC	CGI	GCC	TGC	CCTG	420
	V	P	T	L	E	E	L	N	L	S	Y	N	S	Ι	T	T	V	P	A	L	
421	α	CGA(CTC	CCT	CGT	GTC	CCT	GTC	GCT	GAG	CCG	CAC	CAA	CAT	CCI	'GGT	GCI	'AGA	CCO	CACC	480
	P	D	S	L	V	S	L	S	L	S	R	T	N	I	L	V	L	D	P	T	
481	CA	CCT	CAC	TGG	CCT	ACA	TGC	∞ I	GCG	CTA	CCT	GTA	CAT	'GGA	TGG	CAA	CTG	CTA	CTA	CAAG	540
	Н	L	T	G	L	H		_		Y	L	Y	M	D	G	N	С	Y	Y	K	
541	AA																		CAA	CCTC	600
		P		_									A						N	L	
601	AC	ACA:	ICT	CTC	ACT	CAA	GTA	CAA	CAA	TCT	CAC	GGA	.GGT	'GCC	CCG	CAG	CCI	GCC	CCO	CAGC	660
	T	Н	_	•	_	K	_	N		L	_	_	V	_		•	_	_	P	S	
661										CCA	CAT	TGT	CAC	CCT	GAC	GCC	TGA	.GGA	CCT	GGCC	720
		_	_	_	_	L	_	_		Н	I	•	T		_	P		D	_	A	
721	AA'	ICT(GAC	TGO	CCT	GCG	CGT	GCT	'TGA	TGT	GGG	GGG	GAA	CTG	CCG	XXX	CTG	TGA	CCA	TGCC	780
	N	L	T	<u>A</u>	L	R	V	L	D	V	G	G	Ŋ	C	R	R	<u>C</u>	D	<u>H</u>	<u>A</u>	

781	Œ	CAA	$\overline{\mathfrak{m}}$	CTG	CAG	GGA	GTG	CCC.	AAA	GGA	CCA	CCC	CAA	GCT	GCA	CTC	TGA	CAC	CTT	CAGC	840
	R	N	P	С	R	E	С	P	K	D	H	P	K	L	Н	S	D	T	F	S	
841	CA	CCT	GAG	CCG	CCT	CGA	AGG	CCT	GGT	GTT	GAA	AGA	CAG	TTC	TCT	CTA	CAA	CCT	GGA	CGCC	900
	Н	L	S	R	L	Ε	G	L	Λ	L	K	D	S	S	L	Y	N	L	D	A	
901	AG	GTG	GTT	CCG	AGG	CCT	GGA	CAG	GCT	CCA	AGT	GCT	GGA	CCT	GAG	TGA	GAA	CTT	CCT	CTAC	960
	R	W	F	R	G	L	D	R	Ľ	Q	V	L	D	L	S	E	N	F	L	Y	
961	GA	CTG	CAT	CAC	CAA	GAC	CAC	GGC	CTT	CCA	.GGG	CCT	GGC	CCG	ACT	`gŒ	CAA	CCT	CAA	CCTG	1020
	D	C	Ι	T	K	T	T	A	F	Q	G	L	A	R	L	R	K	L	N	L	
1021	TC	CTT	CAA	TTA	CCA	CAA	GAA	GGT	GTC	CTT	TGC	CCA	CCT	GCA	CCT	GGC	'ACC	CTC	CTT	TGGG	1080
	S	F	N	Y	Н	K	K	V	S	F	A	Н	L	Н	L	A	P	S	F	G	
1081	CA	CCT	Œ	GTO	CCT	GAA	GGA	CCT	GGA	CAT	GCA	TGG	CAT	CTT	CTT	CCG	CTC	GCT	CAG	TGAG	1140
	Н	L	R	S	L	K	Ε	L	D	M	Н	G	I	F	F	R	S	L	S	E	
1141	AC	CAC	GCT	CCA	ACC	TCT	GGT	CCA	ACT	GCC	TAT	GCT	CCA	GAC	CCT	GCG	CCT	GCA	GAT	GAAC	1200
	T	T	L	Q	P	L	V	Q	L	P	M	L	Q	T	L	R	L	Q	M	N	
1201																					1260
													F								
1261																					1320
	L	•	_										V								
1321																		'GGA	CAC	TCTC	1380
	G	R 	E	R	V	M		Р				•	A					D	T	L	
1381																			GTC	TCGG	1440
			_	D	_								S				D	_	S	•	:
1441																				CCTG	1500
	N	N	L	-	T		_						R							L	
1501																	TGI	GCC	GCT	GACC	1560
	R	\underline{L}	<u>S</u>	H	N	<u>S</u>	<u> I </u>	<u>S</u>	Q	A	V	N	G	<u>S</u>	Q	F	V	P	L	_T	

1561	AG	CCT	GCG	GGT	GCT	GGA	CCT	GTC	CCA	CAA	CAA	GCT	GGA	CCT	GTA	TCA	CGG	GCG	CTC	GTTC	1620
	S	L	R	V	L	D	L	S	Н	N	K	L	D	L	Y	Н	G	R	S	F	
1621	AO	GGA	GCT(GCC	GCG	CCT	GGA	AGC	ACT	'GGA	CCT	CAG	CTA	CAA	CAG	CCA	GCC	CTT	TAC	CATG	1680
	T	E	L	P	R	L	E	A	L	D	L	S	Y	N	S	Q	P	F	T	M	
1681	CA	GGG	IGI	GGG	CCA	CAA	CCT	CAG	CTT	ŒŢ	GGC	CCA	GCT	GCC	CGC	CCT	GCG	CTA	CCT	CAGC	1740
	Q	G	V	G	Н	N	L	S	F	V	A	Q	L	P	A	L	R	Y	L	S	
1741	CT	GGO	GCA(CAA	TGA	CAT	CCA	TAG	CCG	AGT	GTC	CCA	GCA	CT.	CIG	TAG	CGC	CTC	ACT	GTGC	1800
	_	A		N	D	I	Н					_	_	L					-		-
1801	GO	CCT	GGA(CTT	TAG																1860
	A	_	D 	F	_									A				_	_	_	_
1861																					1920
1,001	R	-	F	_									_	L	_		N	Н	_	Н	1000
1921																					1980
1001		_						_				-	_	L			_		_	- '	2040
1301	D	CAA N	laa: N		A		_	CAA N						L							2040
20/1		••	•	_		_	_	• '	• •											T	2100
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2101	_	_			_		~					_		-	_	_	_	_		-	2160
2101	_	_	_		_	_	_	_			_			F							2100
2161	_					_	_	_	_	-	_	_	_	-				_	_	-	2220
														N							
2221	CC	CTC	CTG	GTT	TGG	CTC	GAT	GGT	GGG	CAA	CCT	GAA	AGT	ŒΊ	'AGA	CGI	GAG	CGC	CAA	.CCCT	2280
	Р	S	W	F	G	S	M	V	G	N	L	K	V	L	D	V	S	A	N	P	
2281	CT	GCA	CTG	CGC	CTG	TGG	G GC	GAC	CTI	ŒI	GGC	CTT	CCI	GCI	'GGA	.GGT	ACA	.GGC	TGC	CGTG	2340
	L	Н	С	A	С	G	A	T	F	V	G	F	L	L	Ε	V	Q	A	A	V	

P G L P S R V K C G S P G Q L Q G H S I 2401 TTTGCGCAAGACCTGCGCCTCTGCCTGGATGAGACCCTCTCGTGGAACTGTTTTGGCATC	
	-
2401 TTTGCGCAAGACCTGCGCCTCTGCCTGGATGAGACCCTCTCGTGGAACTGTTTTGGCATC	
	2460
FAQDLRLCLDETLSWNC <u>FGI</u>	
2461 TCGCTGCTGGCCATGGCCCTGGGCCTGGTTGTGCCCATGCTGCACCACCTCTGCGGCTGG	2520
S L L A M A L G L V V P M L H H L C G W	
2521 GACCTCTGGTACTGCTTCCACCTGTGCCTGGCCTGCCCCACCGAGGGCAGCGGCGG	2580
D L W Y C F H L C L A W L P H R G O R R	
2581 GGCGCAGACGCCCTGTTCTATGATGCCTTCGTGGTCTTTGACAAAGCTCAGAGTGCTGTG	2640
GADALFYDAFVVFDKAQSAV	
2641 GCCGACTGGGTGTACAACGAGCTGCGGGTGCAGCTGGAGGAGCGCCGTGGGCGCGCGC	2700
A D W V Y N E L R V Q L E E R R G R R A	2,00
2701 CTGCGCCTGTGCCTGGAGAGCGAGACCTGGTTACCTGGCAAGACGCTCTTCGAGAACCTG	2760
	2100
	2020
2761 TGGCCTCAGTCTACAGCAGCCGCAAGACCCTGTTTGTGCTGGCCCACACGGACCGTGTC	2820
WASVYSSRKTLFVLAHTDRV	
2821 AGCGGCCTCTTGCGTGCCAGTTTCCTGCTGGCCCAGCAGCGCCTGCTGGAGGACCGCAAG	2880
SGLLRASFLLAQQRLLEDRK	
2881 GACGTTGTAGTGCTGGTGATCCTGCGCCCCGATGCCTACCGCTCCCGCTACGTGCGCCTG	2940
D V V V L V I L R P D A Y R S R Y V R L	
2941 CGCCAGCGCCTCTGCCGCCAGAGTGTCCTCCTCTGGCCCCACCAGCCCCGTGGGCAGGGC	3000
RQRLCRQSVLLWPHQPRGQG	
3001 AGCTTCTGGGCCCAGCTGGCCACAGCCCTGACCAGGGACAACCGCCACTTCTATAACCGG	3060
S F W A Q L G T A L T R D N R H F Y N R	
3061 AACTTCTGCCGGGGCCCCACGACAGCCGAATAG 3093	
NFCRGPTTAE*	

FIG. 5



SWINE	1	MCPRCTLHPLSLLVQVTALAATLAQCRLPAFTLPCELQPHGLVNCNWLFLKSVPHFSAA	58	SWINE
HUMAN	1	MCF-CRSALHPLSLLVQAIMLAMTLALGTLPAFLPCELQPHGLVNCNWLFLKSVPHFSMA	5 9	HUMAN
MOUSE	1	MVLRRRT-LHPLSLLVQAAVLAETLALGTLPAFLPCELKPHGLVDCNWLFLKSVPRFSAA	59	MOUSE
CAT	1	MCP-CHGALHPLSLLVQAAALAVALAQGTLPAFLPCELQRHGLVNCDWLFLKSVPHFSAA	59	CAT
		* ******** ** ** ** ******** ** * * ****		
SWINE	59	APRANVTSLSLLSNRIHHLHDSDFVHLSSLRTLNLKWNCPPAGLSPMHFPCHMT1EPNTF	118	SWINE
HUMAN	60	APROVVTSLSLSSNRIHHLHDSDFAHLPSLRHINLKWNCPPVGLSPMHFPCHMTIEPSTF	119	HUMAN
MOUSE	60	ASCONITRLSLICARIHHLHASDEVHLSALRQUALKWACPPTGLSPLHFSCHMTIEPRTF	119	MOUSE
CAT	60	APRONVTSLSLYSNRIHHLHDSDFVHLSSLRRINLKWNCPPASLSPMHFPCHMTIEPHTF	119	CAT
		* . * . * * * * * * * * * * * * * * * *		
SWINE	119	LAVPTLFELNLSYNSTTIVPALPDSLVSLSLSRINILVLDPTHLTGLHALRYLYMDGNCY	178	SWINE
HUMAN	120	LAVPTLEEINLSYNNIMIVPALPKSLISLSLSHTNIIMLDSASLAGLHALRFLFMDQNCY	179	HUMAN
MOUSE	120	LAMRITLEELNLSYNGITTVPRLPSSLVNLSLSHTNILVLDANSLAGLYSLRVLFMDQNCY	179	MOUSE
CAT	120	LAVPTLFELNLSYNSITTVPALPSSLVSLSLSRINILVLDPANLAGLHSLRFLFIDGWCY	179	CAT
}		** ******** * *** ** ** *** *** * * * *		
SWINE	179	YKNPCQCALEVVPGALLGLGNLTHLSLKYNNLTEVPRSLPPSLETLLLSYNHIVTLTPED	238	SWINE
HUMAN	180	YKNPCRQALEVAPGALLGLGNLTHLSLKYNNLTVVPRNLPSSLEYLLLSYNRIVKLAPED	239	HUMAN
MOUSE	180	YKNPCTGAVKVTPGALLGLSNLTHLSLKYNNLTKVPRQLPPSLEYLLVSYNLIVKLCPED	239	MOUSE
CAT	180	YKNPCPQALQVAPGALLGLGNLTHLSLKYNNLTAVPRGLPPSLEYLLLSYNHLITLAPED	239	CAT
		***** * * ******* ******* *** ** ** * *		
SWINE	239	LANLTALRVLDVGGNCRRCDHARNPCRECPKDHPKLHSDTFSHLSRLEGLVLKDSSLYNL	298	
HUMAN	240	LANLTALRVLDVGGNCRRCDHAPNPCMECPRHFPQLHPDTFSHLSRLEGLVLKDSSLSWL	299	
MOUSE	240	LANLTSLRVLDVGQVCRRCDHAPNPCIECCQKSLHLHPETFHHLSHLEGLVLKDSSLHTI	299	
CAT	240	LANLITALRVLDVGGNCRRCDHARNPCMECPKGFPHLHPDTFSHLNHLEGLVLKDSSLYNI	299	
		***** *********** *** ** ** ** ** ** **		

SWINE	299	DARWFRGLDRLQVLDLSENFLYDCITKTTAFQGLARLRKLNLSFNYHKKVSFAHLHLAPS 3	358
HUMAN	300	NASWFRGLGNLRVLDLSENFLYKCITKTKAFQGLTQLRKLNLSFNYQKRVSFAHLSLAPS 3	359
MOUSE	300	NSSWFQGLVNLSVLDLSENFLYESINHINAFQNLTRLRKLNLSFNYRKKVSFARLHLASS 3	359
CAT	300	NPRWFHALGNLMVLDLSENFLYDCITKTTAFQGLAQLRRLNLSFNYHKKVSFAHLHLAPS 3	359
		** * * ******** * * *** * ** ***** * * *	
SWINE	359	FGHLRSLKELDMHGIFFRSLSETTLQPLVQLPMLQTLRLQMNFINQAQLSIFGAFPGLLY 4	118
HUMAN	360	FGSLVALKELDMHGIFFRSLDETTLRPLARLPMLQTLRLQMNFINQAQLGIFRAFPGLRY 4	119
MOUSE	360	FKNLVSLQELMMGIFFRSLNKYTLRWLADI.PKLHTLHLQMNFINQAQLSIFGIFRALRF 4	119
CAT	360	FGSLLSLQQLDMHGIFFRSLSETTLRSLVHLPMLQSLHLQMNFINQAQLSIFGAFPGLRY 4	119
		* * * * * * * * * * * * * * * * * * * *	
SWINE	419	VDLSDNRISGAARPVAITREVDGR-ERVWLPSRNLAPRPLDTLRSEDFMPNCKAFSFTLD 4	477
HUMAN	420	VDLSDNRISGASELTATMGEADGG-EKVWLQPGDLAPAPVDTPSSEDFRPNCSTLNFTLD	478
MOUSE	420	VDLSDNRISGPSTLSEATPEEADDAEQEELLSADPHPAPLSTPASKNFMDRCKNFKFTMD 4	179
CAT	420	VDLSDNRISGAMELAAATGEVDGG-ERVRLPSGDLALGPPGTPSSEGFMPGCKTLNFTLD 4	478

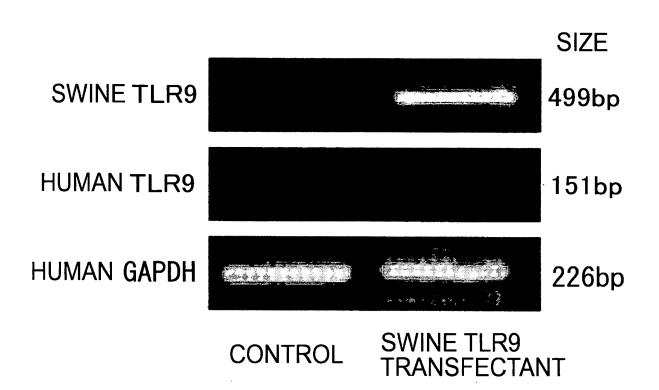
SWINE	478	LSRNNLVTIQSEMFARLSRLECLRLSHNSISQAVNGSQFVPLTSLRVLDLSHNKLDLYHG	537
HUMAN	479	LSRNNLVIVOPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQVLDLSRNKLDLYHE	538
MOUSE	480	LSRNNLVTIKPEMEVNLSRLQCLSLSHNSIAQAVNGSQFLPLINLQVIDLSHNKLDLYHW	539
CAT	479	LSRNNLVTIQPEMFARLSRLQCLLLSRNSISQAVNGSQFMPLTSLQVLDLSHNKLDLYHG S	538
		******* ** ** * * * * * * * * * * * * *	
L			

	SWINE	538	RSFIELP	RLEAI	DLSY	NSOPF	IMQG\	IGHNL	SFVAQ	LPALR	YLSLA	HIDIH	SRVS	QUCSA	597
	HUMAN	539	HSFTELP	RLEAI	DLSY	NSOPF		JGHNF:	SFVAH	LRTLR	HLSLA	HINNIH	SQVS	QLCT	598
	MOUSE	540	KSFSELP	QLQAI	DLGY	NSOPF	SIKG	IGHNF:	SFVAH	LSMLH	SLSLA	HNDIH	TRVS	SHLNSN	599
	CAT	539	RSFTELP	RLEAI	DLSY	NSQPF:	SMQG	VGHNL.	SFVAQ	LPALR	YLSLA	HIDIH	SRVS	QQLCSA	598
			.*	.*.**	***.*	****	*	***	***	* *.	***	** **	**	*.*	
	SWINE	5 98	SLCALDF	SGNDI	SRMW	AEGDL.	YLRFI	QGLR.	SLVWL	DLSQN	HLHM	LPRAL	DNLP	KSLKHL	657
	HUMAN	599	SLRALDF	SGVAI	GHM	AEGDL	YLHFI	WIS	GLIWL	DLSQN	RLHII	LPQTL	RNLP	KSLQVL	658
	MOUSE	600	SVRFLDF	SGVQ	GRM	DEGGL:	YLHFI	QGLS	GLLKL	DLSQN	NLHII	RPONL	DNLP	KSLKLL	659
	CAT	599	SLRALDF	SGNAI	SRMW	AEGDL)	YLXFI	RGLR	SLVRL	DLSQN	RLHII	LPRIL	DNLP	KSLRLL	658
			* * * *	*** .	**	***	** *1	* * *	* *	****	**.*	* *	.***	*** *	
	SWINE	658	HLRDNNL	AFFN	SSLT	LLPKL	ETLDI	(AGVQ	LKALS	NGSIP	SGTQI	RRLDL	SGNS	IGEVNP	717
	HUMAN	659	RLRDNYL	AFFKV	WSLH	FLPKL	EVLDI	LAGNR	LKALT	NGSLP.	AGTRI	RRLDV	SONS	ISFVAP	718
	MOUSE	660	SLRDNYL	SFFN	VISLS	FLPNL	EVLD1	LAGVQ	LKALT	NGTLP	NGILI	ØKIDV	SSNS	IVSVVP	719
	CAT	659	RLRDNYL	AFFN	VSSLV.	LLPRL	EALDI	LAGVQ	LKALS	NGSLP:	NGIQI	QRLDL	SSNS	ISFVAS	718
		•	****	.**.	* **	** *	* **1	****.	****	**.**	** *	**	* **	* .* .	
	SWINE	718	GFFALAK	QLEEI	INLSA	NALKT	VEPSI	WEGSM	VGNT K	VLDVS	ANPLE	ICACGA	TFVG	FLLEVQ	777
	HUMAN	719	GFFSKAK	ELREI	INLSA	NALKT	VDHS	WFGPL	ASALQ	ILDVS	ANPL	iCACGA	AFMD	FLLEVQ	778
	MOUSE	720	AFFALAV	ELKE	VNLSH	NILKT	VDRSI	WFGPI	VMNLT	VLDVR	SNPLE	ICACGA	AFVD	LLLEVQ	779
	CAT	719	SFFALAT	RLREI	LNLSA	NALKT	VEPS	WFGSL	AGTIK	VLDVI	GN BTI	I CACGA	AFVD	FLLEVQ	778
			***	* *	.***,	* * * * *	* *	***	*	***	***	****	.*	.****	
1	SWINE	778	AAVPGLI	PSRVK	CGSP(QLQGH	SIFA	QDLRI	CLDET	LSWN	FGIS	LLAMAI	GLV	PMLHHL	837
	HUMAN	779	AAVPGLI	PSRVK	CGSP(QLQGI	SIFA	QDLRI	CLDEA	LSWDC	FALS	LLAVAI	GLG\	PMLHHL	838
	MOUSE	780	TKVPGL	NGVK	CGSPC	QLQ T	SIFA	QDLRI	CLDEV	LSWDO	FGLS	LLAVA	MM	PILHHL	839
	CAT	779	AAVPGLI	PGHVK	CGSPC	DLQG	SIFA	QDLRI.	CLDEA	LSWDO	FGLS	LLTVAI	GLAV	PMLHHL	838
			****	**	****	***	***	****	***	*** *	* * *	** . *	* *	* * * * * *	

SWINE	838 CGWDLWYCFHLCLAWLPHRGQRRGADALFYDAFVVFDKAQSAVADWYNELRVQLFER	895
HUMAN	839 CGWDLWYCFHLCLAWLPWRCRQSCRDEDALPYDAFVVFDKTQSAVADWVYNELRGQLEEC	898
MOUSE	840 CGWDVWYCFHLCLAWLPLLARSRRSAQA-LPYDAFVVFDKAQSAVADWYNELRVRLEGR	898
CAT	839 CGWDLWYCFHLCLAWLPRRGRRGADALPYDAFVVFDKAQSAVADWVYNELRVRLFER	896
	**** ********	
SWINE	896 RGRRALRICLEERDWLPGKTLFENLWASVYSSRKTLFVLAHTDRVSGLLRASFILLAQORL	955
HUMAN	899 RGRWALRLCLEERDWLPGKTLFENLWASVYGSRKTLFVLAHTDRVSGLLRASFLLAQQRL	958
MOUSE	899 RGRRALRICLEDROWLPGQILFENLWAS IYGSRKTIFVLAHTDRVSGILRTSFILLAQQRL	958
CAT	897 RGRRALRICLEERDWLPGKTIFENLWASVYSSRKMLFVLAHTDRVSGLLRASFILLAQQRL	956
	*** ****** ***** ****** * *** ******** *	
SWINE	956 LEDRKDVVVLVILRPDAYRSRYVRLRORLCROSVLLWPHOPROQGSFWAQLGTALTRDNR	1015
HUMAN	959 LEDRKOVVVLVILSPDGRRSRYVRLRQRLCRQSVLLWPHQPSGQRSFWAQLGVALTRDNH	1018
MOUSE	959 IEDRKOVVVLVIIRPDAHRSRYVRLRORLCROSVLFWPQOPNGQGGFWAQLSTALTRONR	1018
CAT	957 LEDRKDVVVLVIIRPDAHRSRYVRLRORLCROSVLLWPHOPSGORSFWAQLGTALTRDNO	1016

SWINE	1016 HFYNRNFCROPTTAE	1030
HUMAN	1019 HFYNRNFCQCP-TAE	1032
MOUSE	1019 HFYNONFCROP-TAE	1032
CAT	1017 HFYNONFCROPTTAE	1031
	**** *** **	

FIG. 10



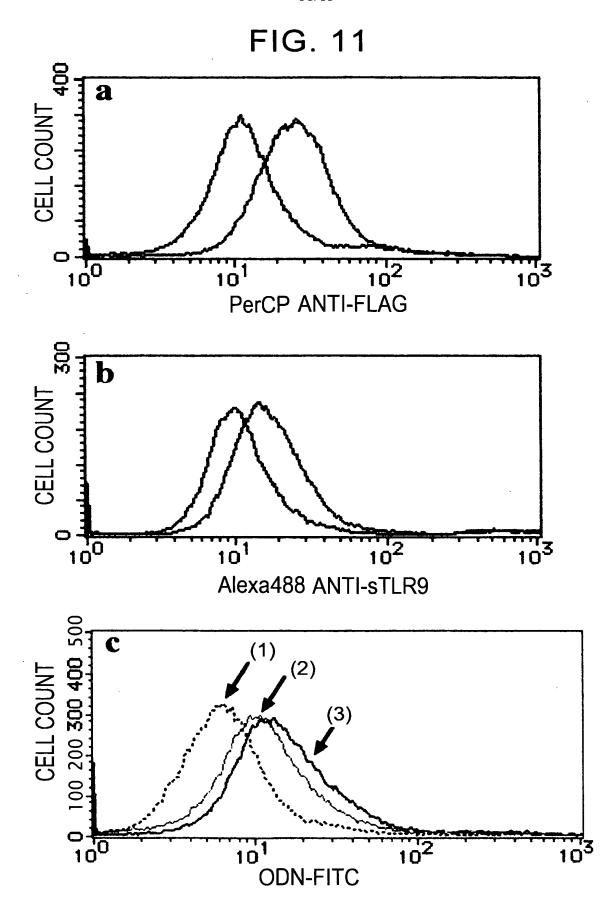


FIG. 12

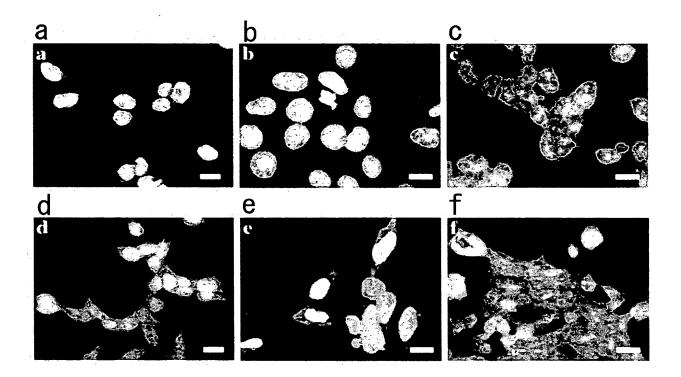


FIG. 13

